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File

 Fe 1: CAD58967. Disease resistanc...[gi:26986180]

BLINK, Domains, Links

LOCUS CAD58967 318 aa linear PLN 15th DEC 2002
DEFINITION Disease resistance protein NBS-LRR type [Musa acuminata].
ACCESSION CAD58967
VERSION CAD58967.1 GI:26986180
DBSOURCE embl locus MAC534312, accession AJ534312.1
KEYWORDS
SOURCE Musa acuminata
ORGANISM Musa acuminata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.
REFERENCE 1 (residues 1 to 318)
AUTHORS Arango,R., Rodriguez,E. and May,G.D.
TITLE Partial cloning of a disease resistance gene analog from Musa
acuminata (Var. Grand Nain)
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 318)
AUTHORS Arango,R.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-2002) Grupo de Biotecnologia Vegetal UNALMED-CIB,
Carrera 72 A No. 78B- 141, Medellin, Antioquia, COLOMBIA
FEATURES Location/Qualifiers
source 1..318
/organism="Musa acuminata"
/cultivar="Grand Nain"
/db_xref="taxon:4641"
Protein 1..318
/product="Disease resistance protein NBS-LRR type"
Region 137..>304
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/note="NB-ARC"
/db_xref="CDD:24492"
CDS 1..318
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/coded_by="AJ534312.1:<1..957"
/db_xref="GOA:Q8GUB6"
/db_xref="UniProt/TrEMBL:Q8GUB6"
ORIGIN
1 vhdeiketlt acfqrlrrtrn sltealsdlr ataqrvkdkv eeeeahqric npdvrrwqkk
61 vdeilrecda ggeheepkrc aclcgcdmdl lhrhrvarkv vqnlgdvnkl ksdgdaftpp
121 fnhepppepv eelpfetqtgmi gmelalsql srfdeaeksi ighvhglggvg ktllktlnn
181 elkentrdyh vvimievans etlnvvdmqk iianrlalpw neseterers tylrralrrk
241 kfvvvllddw kkfqladvgi ptpssdkgck lilasrsnqv cvemgdkepm empclgdnes
301 lrlfpeqldg rgqcrhrp
//

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Oct 4 2004 14:35:49

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Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000! wordsize: 3

Filter

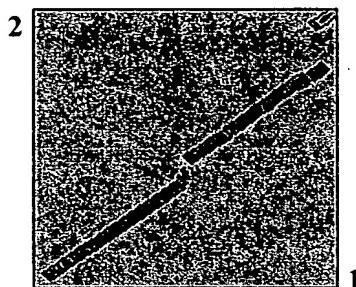
Prior art

claimed

Sequence 1 lcl|seq_1 Length 918 (1 .. 918)

D1 SEQ ID NO: 42 x SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 389 bits (999), Expect = e-106

Identities = 303/949 (31%), Positives = 448/949 (46%), Gaps = 139/949 (14%)

Query: 42 AVLEDAQEQLNDKPLENWLQKLNAATYEVDDILDEYKTKATRF--LQSEYGRYHPKVI- 98
++LE+A+ +++ DK L WL +L Y+ DDILDEY+ A R +S + R VI

Sbjct: 52 SLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAIRLKVTRSTFKRLIDHVII 111

Query: 99 --PFRHKVGKRMMDQVMKKLNAAEERK-NFHLQEKKIERQAATRE-TGSVLTEPVQVYGRD 154
P HKV + K+LN + ER+ N E + R T S+LTE + GR

Sbjct: 112 NVPLAHKVA---DIRKRLNGVTLERELNLGALEGSQPLDSTKRGVTTSLTESCIVGRA 167

Query: 155 KEKDEIVKILINNVSDAQKLSVLPILGMGGLGKTTLSQMVFNDQRVTERFYPKIWICVSD 214
++K+ +--+L+ A + V+PI+G+GG GKTTLSQ++FND+RV E F ++W+CVSD

Sbjct: 168 QDKENLIRLLLEPSDGA--VPVVPIVGLGGAGKTTLSQLIFNDKRVEEHFPLRMWVCVSD 225

Query: 215 DFDEKRLIKAIVE-SIEGKSLSDMDLAPLQKKLQELLNGKRYFLVLDVWNEDQHKWANL 273
DFD KR+ + I E + G+ + +L LQ L+E + G + LVLDVWNED KW +L

Sbjct: 226 DF DVKRITREITEYATNGRFMDLTNLNMLQVNKEEIRGTTFLVLDDVWNEDPVWKESL 285

Query: 274 RAVLKVGASGAFVLTTTRLEKVGSI MGT LQPYELS NLSPEDCWFLFMQRAGHQ--EEIN 331
A L G G+ V+ TT+ +KV + GT++PY L L+ +D W L +F N

Sbjct: 286 LAPLDAGGRGSVIVTTQSKKVADVTGTM EPYVLEELTEDDSWSLIESHSFREACSSTN 345

Query: 332 PNLVAIGKEIVKKCGGVPLAAKTLGGILRKFREEREWEHV-DSPIWNLPQDESSILPALR 390
P + IG++I KK G+P A +G LR K E W V ++ W +P S +L ALR

Sbjct: 346 PRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWREVLETETWEMPPAADVLSALR 405

Query: 391 LSYHHLPLDLDQCFVYCAVFPKDTKMAKENLIAFWMAHGFLLSKG NLELEDV----- 442
SY +LP L CF +CA+F K + K+ LI W+A + S + ED+

Sbjct: 406 RSYDNLPPQLKLCFAFCALFTKGYRFRKD TLIH MWIAQNL IQSTESKRSEDMAEECFDDL 465

Query: 443 -----NEVWNEL-----YLRVSSYSPSLLQK----- 463
N V N+ Y R SP + K

Sbjct: 466 VCRFFFYRYSWGNVNMNDSVHDLARWVS LDEYFRADEDSP LHIS KPIR HLS WC SERITNV L 525

Query: 464 -----FXXXXXXXXXXXXQLPSSI 484
LPSS+

* Sbjct: 526 EDNNNTGGDAVNPLSSLRLLFLGQSEFRSYHLLDRMFRMLSRIRVLDNSNCVIRNLPSSV 585

Query: 485 GDLVHLRYLDLSGNFRIRNLPKRLCKLQLQTLSDLHYCDSLSCLPKQTSLGSLRNLLD 544
G+L HRLYL LS N RI+ LP+ + L QRTL L C+ L LP+ S+L LR L +

Sbjct: 586 GNLKHLRYLGLS-NTRIQRLPESVTRLCLLQTLLEGCE-LCRLPRSMSRLVKLRQLKAN 643

Query: 545 GCSLTSTPPRIGLLTCLKSLSFCVIGKRKGYQLGELKNLN-LYGSISITKLDdrvKKDSDA 603
+ + + + G L L+ L + + K+KG+ + EL +N L+G +SI L V+K ++

Sbjct: 644 P-DVIADIAKVGRLIELQELKAYNVDKKGHGIAELSAMNQLHGDLSIRNLQNVEKTRES 702

Query: 604 KEANLSAKANLHSCLSWLDGKHR---YDSEVLEALKPHSNLKYLEINGFGGIRLPDW 659
++A L K L L W DG+ D +VL+ L+PH NL+ L I +GG P W

Sbjct: 703 RKARLDEKQKLKLLDLRW-ADGRGAGECDRDRKVLKGLRPHPNLRELSIKYYGGTSSPSW 761

Query: 660 MNQSVLKNNVSIRIRGCENCSCLPPFGEPCLESLELHTGSADVEYVEDNVH---PGRF 715
M L N+ +IR+R C + LP G+L L L + G + V + + F

Sbjct: 762 MTDQYLPNMETIRLRSCARLTELPCLGQLHILRHLCI-DGMSQVRQINLQFYGTGEVSGF 820

Query: 716 PSLRKLVIWDFSNLKGLLK-KEGEEQFPVLEEMTFYWCP-MFVIPTLSSVKTLKVIATDA 773
P L L I +L+ + + FP L ++ CP + +P+L TL+ +

Sbjct: 821 PLLELLNIRRMPGLEEWSEPRRNCCYFPRLHKLLIEDCPRLRNLPSP--PTLEELRISR 878

Query: 774 TVLRSISNLRALTSLDISNNVEATSLPEEMFKSLANLKYLNISFFRNLKELPTXXXXXX 833
T L + + D++ NV +SL + L +L + NL L T

Sbjct: 879 TGLVDLPGFHG--NGDVTTNVSLSSLHVSECRLSLSEGLLQ--HNLVALKT----- 927

Query: 834 XXXXXFEFCNALESPLPAEGVKGLTSLTELSVSNCMMLKC---LPEGLQH 879
F C++LE LPAEG + SL L ++NC L C LP L+H

Sbjct: 928 ---AAFTDCDSLEFLPAEGFRTAISLESLIMITNC-PLPCSFLLPSSLEH 972

Score = 43.9 bits (102), Expect = 0.036

Identities = 24/75 (32%), Positives = 37/75 (49%), Gaps = 1/75 (1%)

Query: 842 CNALESPLPAEGVKGLTSLTELSVSNCMMLKCLPEGLQHXXXXXXXXQCPIVKRCERGI 901
C LE LPA ++ L SL+ L + C + PG +CP + +RC+

Sbjct: 1148 CPNLEVLPAN-LQSLCSLSTLYIVRCPRIHAFPPGGVMSLAHLVIHECPQLCQRCDPG 1206

Query: 902 GEDWHKIAHIPYLT 916

G+DW IA++P + L

Sbjct: 1207 GDDWPLIANVPRICL 1221

CPU time: 0.16 user secs. 0.00 sys. secs 0.16 total secs.

Lambda	K	H
0.320	0.137	0.410

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 7820

Number of extensions: 5118

Number of successful extensions: 24

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 7

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 918

Length of database: 765,028,816

Length adjustment: 140

Effective length of query: 778

Effective length of database: 765,028,676
Effective search space: 595192309928
Effective search space used: 595192309928
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 81 (35.8 bits)



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3

Filter Align

Prior art

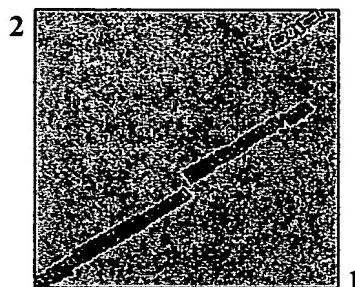
claimed

Sequence 1 lcl|seq_1 Length 918 (1 .. 918)

D1

SEQ ID NO: 42 x SEQ ID NO: 2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 375 bits (964), Expect = e-102

Identities = 286/950 (30%), Positives = 437/950 (45%), Gaps = 155/950 (16%)

Query: 2 AEAIFIQVVLNDNLTSFLKGELVLLFGFQDEFQ-LSSMFSTIQAVALEDAQEKLNDKPLEN 59
A++FIQ +LD ++ +L G D+ + L + I A+A+ A+ + + L

Sbjct: 12 AQSFQTLDDKASNCAIQQLARRRGLHDDLRLRTSLLRIHAILDKAETRWNHKNTSLVE 71

Query: 60 WLQKLNAATYEVDDILDEYKTAKTRFLQSEYGRYHPKVIPFR-----HKVGKR 107
+++L A Y+ +D+L+E + +A + G + F G R

Sbjct: 72 LVRQLKDAAAYDAEDLLEELEYQAAKQKVEHRGDQISDLFSFSLSTASEWLGADGDDAGTR 131

Query: 108 MDQVMKKLNIAIAEERKNFHQL-----EKIIERQAATRETGSVLTEPVQVYGRDKEKDEIV 161
+ ++ KL IA + + + + RET S LTE V+GRD+E+++V

Sbjct: 132 LREIQGKLCNIAADMMMDVMQLLAPDDGGRQFDWKVVRRETSSLTETVVFGRDQEREKVV 191

Query: 162 KILINNSVDAQKLSVLPILGMGGLGKTTLSQMVNDQRVTERFYPKIWICVSDDFDEKRL 221
++L+++ S SVLP++G+GG+GKTTL+Q+V+ND RV F+ K+W+CVSD+F+ KRL

Sbjct: 192 ELLLDSGSGNSSFVPLVIGGGVGKTTLAQLVYNDNRVGNYFHLKVWVCVSDNFNVKRL 251

Query: 222 IKAIVESIEGKSLSD-MDLAPLQKQLQELLNGKRYFLVLDVWNEDQHKWANLRAVLKVG 280
K I+ES SD ++L LQ+ L+E + +R+ LVLDVW+E++ W L A L+

Sbjct: 252 TKEIIIESATKVEQSDKLNLDLQQILKEKIASERFLLVLDVWSENRRDDWERLCAPLRFA 311

Query: 281 ASGAFVLTTRLEKVGSIIMGTLPQYELSNLSPEDCWFLFMQRAGHQEEINP---NLVA 336
A G+ V+ TTR K+ SI+GT++ L L + W LF + AFG +NP L

Sbjct: 312 ARGSKVIVTTRDTKIASIIGTMKEISLDGLQDDAYWELFKKCAF---SVNPQEHLLEV 368

Query: 337 IGKEIVKKCGGVPLAAKTLGGILRFKREEREWEHV-DSPIWNLPQDEESSILPALRLSYHH 395
IG++I K G PLAATLG +LR + W + +S +W LPQ E+ ILP L LSY H

Sbjct: 369 IGRKIAGKLKGSPPLAAKTLGSLLRLDVSQEHWRTIMESEVWQLPQAENEILPVLWLSYQH 428

Query: 396 LPLDLDQCFVYCAVFPKDTKMAKENLIAFWMAHGFLLSKGNLELEDV----NEVWNELY 450
LP L QCF +CAVF KD K LI W+A GF+ +GN +EDV +E+ N +

Sbjct: 429 LPGHLRQCFAFCAVFKDYLFYKHELIQTWIAEGFIAHQGNKRMEDVGSSYFHELVNRSF 488

Query: 451 LRVSSY----- 456
+ S +

Blast Result

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Sbjct: 489 FQESRWRGRYVMHDLIHDLAQFISVGECRIRDDKSKEPSTTRHLSVALTEQMKLVD 548

Query: 457 -----SPSLLQKFXXXXXXXXXXXXXQLPSSIGDLV 488
SL ++ +LP IGDL+

Sbjct: 549 GYNKLRTLMINNQRNQYPYMTKVNSCLPHSLFKRLKRIHVVLQKCGMKELPDIIGD 608

Query: 489 HLRYLDLSGNFRIRNLPKRLCKLQNLQTLDLHYCDSLSCLPKQTSKLGSLRNLLDGCS 548
LRYLD+S N I+ LP+ LC L NLQ L L C L P+ SKL +LR L ++ +

Sbjct: 609 QLRYLDISYNACIQRLPESLCDLYNLQALRLWGC-QLRSFPQGMSKLINLRQLRVED-EI 666

Query: 549 TSTPPRIGLLTCLKSLSCFVIGKRKGYQLGELKNL-NLYGSISITKLDRVKKDSAKEAN 607
S +G L L+ LS F + G +L EL L L ++ IT L+ V +A +A

Sbjct: 667 ISKIYEVGKLISLQELS AFKVLNNHGNKLAELSGLTQLRSTLRITNLENVGSKEEASKAK 726

Query: 608 LSAKANLHSLCLS-----DLDGKHRYDSEVLEALKPHSNLKYLEINGFGGIRLPDW 661
L K L +L L W L+ + EVL L+PH LK L I G+ G +P W++

Sbjct: 727 LHRKQYLEALELEWAAGQVSSLEHELLVSEEVLLGLQPHFLKSLTIRGYSGATVPSWLD 786

Query: 662 QSVLKNVVSIRIRGCENCSCLPFGELPCLESLELHTGSADVEYVEDNVH-----PGR 714
+L N+ ++++ C L G+LP L+ L+ + V+ H

Sbjct: 787 VKMLPNLGLTLKLENCTRLEGLSYIGQLPHLKVLHMKR---MPVVKQMSHELCGCTKSKL 842

Query: 715 FPSSLRKLVIWDFSNLKGLLKKEGEEQFPVLEEMTFYWCPMFVIPTLSSVKTLKVIATDAT 774
FP L +LV+ D LK +FP L+ +P L+ + A

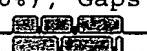
Sbjct: 843 FPRLEELVLEDMPTLK-----EFPNLAQ-----LPCLKIIMKKNMFAVKHI 883

Query: 775 VLRSISNLRALTSDLISNNVEATSLPEEMFKSLANLKYLNISFFRNLKEL 824
++ + L+ V L E +L L+L+ +N+ L

Sbjct: 884 GRELYGDIESNCFLSLEELVLQDMLTLEELPNLQQLPHLKVIHMKNMSAL 933

Score = 38.9 bits (89), Expect = 1.2

Identities = 38/162 (23%), Positives = 66/162 (40%), Gaps = 16/162 (9%)

Query: 718 LRKLVIWDFSNLKGLLKKEGEEQFPVLEEMTFYWCPMFVI---PTLSSVKTLKVIATDAT 774
L++L N GL EG + L+ + CP ++ V +L ++ D T

Sbjct: 1258 LKELGTVRIENCDGLGSIEGLQVLKSLKRLAIIGCPRLLLNEGDEQGEVLSLLELSVDKT 1317

Query: 775 VLRSISNLRALTSDLISNNVEATSLPE-----EMFKSLANLKYLNISFFRNLKELP 825
L +S ++ +L ++++ P+ E+ SL L+ L +NL+ LP

Sbjct: 1318 ALLKLSLIK--NTLPFIHSLRIIWSPQKVMFDLEEQELVHSLTALRRLEFFRCKNLQSLP 1375

Query: 826 TXXXXXXXXXXFEFCNALES LPAEGVKGLTSLTELSVSNC 867
T C ++SLP +G+ T LT+L +C

Sbjct: 1376 TELHTLPSLHALVVSDCPQIQSLPEKGLP--TLLTDLGFDH 1415

CPU time: 0.22 user secs. 0.00 sys. secs 0.22 total secs.

Lambda K H
0.320 0.137 0.410

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 9464

Number of extensions: 6271

Number of successful extensions: 20

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 10

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 918
Length of database: 765,028,816
Length adjustment: 140
Effective length of query: 778
Effective length of database: 765,028,676
Effective search space: 595192309928
Effective search space used: 595192309928
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 81 (35.8 bits)



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Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3

 Filter Align

PRIOR ART

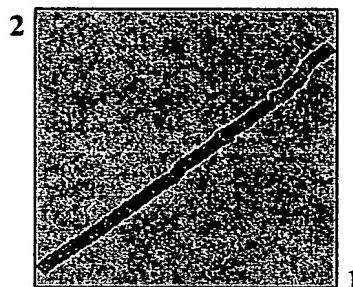
CLAIMED

Sequence 1 lcl|seq_1 Length 942 (1 .. 942)

D1 SEQ ID NO: 43

SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 403 bits (1035), Expect = e-110

Identities = 309/998 (30%), Positives = 486/998 (47%), Gaps = 126/998 (12%)

Query: 23 DDILDDCKTEAARFK--QAVLGRYHPRITFCYKVGKRMKEMMEKLDAIAEERR-NFHLD 79
Sbjct: 82 DDILDEYEAAAIRLKVTRSTFKRLIDHVI-INVPLAHKVADIRKRLNGVTLERELNLGAL 140

Query: 80 ERIIERQAARRQ-TGFVLTEPKVYGREKEEDEIVKILINNVSYSEEVPVLPILGMGGLGK 138
Sbjct: 141 EGSQPLDSTKRGVTTSLTESCIVGRAQDKENLIRLLLEPSDGA--VPVVPIVGLGGAGK 198

Query: 139 TTLAQMFNDQRITERHFNLKIWVCVSDDFDEKRLIKAIIVE-SIEGKSLGDMDLAPLQKKL 197
Sbjct: 199 TTLSQLIFNDKRVEEHFPLRMWVCVSDDFDVKRITREITEYATNGRFMDLTNLNMLQVNL 258

Query: 198 QELLNGKRYFLVLDDVNEDQEKWDLNRAVLKIGASGASILITTRLEKIGSIMGTLQLYQ 257
Sbjct: 259 +E + G + LVLDDVNED KW++L A L G G+ +++TT+ +K+ + GT++ Y
KEEIRGTTFLLVLDDVNEDPVKWESELLAPLDAGGRGSVVIVTTQSJKVADVTGTMEPYV 318

Query: 258 LSNLSQEDCWLLFKQRAFCHQT--ETSPKLMEIGKEIVKKCGGVPLAAKTLGGLLRFKRE 315
Sbjct: 319 L L++D W L + +F + T+P++ EIG++I KK G+P A +G LR K
LEELTEDDSWSLIESHSFREASCSTSNNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHG 378

Query: 316 ESEWEHVRDSEIWNLPQDENSVLPALRLSYHHPLDLRQCFAYCAVFPKDTKIEKEYLIA 375
Sbjct: 379 ES W V ++E W +P + VL ALR SY +LP L+ CFA+CA+F K + K+ LI
ESSWREVLETETWEMPPAASDVLSALRRSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIH 438

Query: 376 LWMAHSFLLSKGNMELEDVGNEVNELYLRSFFQEIEVKSGKTYFKMHDLIHDLY----- 430
Sbjct: 439 +W+A + + S + ED+ E ++++L R FF + + M+D +HDL
MWIAQNLIQSTESTKSSEDMAEECFDDLVCRRFFF-----RYSWGNYVMNDSVHDLARWSL 493

Query: 431 -----XXXXXXXXXXXXIRQI-----NVKDDE----DMMFIVTNYKDMMSIGFSEVV 473
Sbjct: 494 IR + NV +D D + +++ + ++ +G SE
DEYFRADEDSPHLISKPIRHLSWCSERITNVLEDNNTGGDAVNPLSSLRTLLFLGQSEFR 553

Query: 474 SSY-SPSLFKRFVSLRVLNLSNSEFEQLPSSVGDVLHRLYLDLSGNKICSLPKRLCKLQN 532
S + +F+ +RVL+ SN LPSSVG+L HRLYL LS +I LP+ + +L

Sbjct: 554 SYHLLDRMFRMLSRIRVLDFSNCVIRNLPSVGNLKHLRYLGLSNTRIQRLPESVTRLCL 613
 Query: 533 LQTLDLYNCQSLSCLPKQTSKLCRLRNVLDCPLTSMPPIGLLTCLKTLGYFVVGERK 592
 Sbjct: 614 LQTLLLEGCE-LCRLPRSMSRLVKLRQLKANPDVIADI-AKVGRILIELQELKAYNVDKKK 671
 Query: 593 GYQLGELRNLN-LRGAISITHLERVKNDMEAKEANLSAKANLHSLSMSW-DRPNRYESE- 649
 Sbjct: 672 GHGIAELSAMNQLHGDSLIRNLQNVEKTRESRKARLDEKQKLKLLDLRWADGRGAGECDR 731
 Query: 650 EVKVLEALKPHPNLKYLEIIDFCGFCLPDWMNHSQLKNVVSILISGCENCSCLPPFGELP 709
 Sbjct: 732 + KVL+ L+PHPNL+ L I + G P WM L N+ +I + C + LP G+L DRKVLLKGLRPHPNLRELSIKYYGGTSSPSWMTDQYLPNMETIRLRSCARLTELPCLGQLH 791
 Query: 710 CLESLELQDGSVVEYV-----EDSGF-----LTRRRFPSSLRKIHIGGFCNLKGLQR 756
 Sbjct: 792 L L + DG +V + E SGF L RR PSL + + ILRHLHI-DGMSQVRQINLQFYGTGEVSGFPLLELLNIRRMPSELLEWS-----EP 840
 Query: 757 MKGAEQFPVLEEMKISDCPMF-----VFPTLSSVKKLE-----IWGEADAGGXXXXX 803
 Sbjct: 841 + FP L ++ I DCP + PTL ++ G D RRNCYFPRLHKLLIEDCPRLRNLPSPPTLEELRISRTGLVDPFGFHNGDVTTNVSL 900
 Query: 804 XXXXXXXXXKIFS-----NHTVTSLLLEEMFK-----NLENLI----- 834
 Sbjct: 901 + + S H + +L F +LE+LI SLHVSECRELRLSLEGLLQHNLVALKTAATDCDSLEFLPAEGFRTAISLESLIMITNCPL 960
 Query: 835 ---YLSVSFLENLK-----ELPTSLASLNNLKCLDIRYCYAXXXXXXXXXXXX 879
 Sbjct: 961 +L S LE+LK L T +L +L LDI+ C PCSFLLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSFLDIKDCPNLSSFPPGPLCQL 1020
 Query: 880 XXXXXXFVEHCNMLKCLPEGLQHLTTLTSLKIRGCPQL 917
 Sbjct: 1021 + +C L+ + G Q LT+L SL I+ CP+L SALQHLSLVNCQRLQSI--GFQALTSLESLTIQNCPRL 1056

CPU time: 0.09 user secs. 0.00 sys. secs 0.09 total secs.

Lambda K H
0.321 0.138 0.416

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 7971
 Number of extensions: 5184
 Number of successful extensions: 25
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's gapped: 2
 Number of HSP's successfully gapped: 1
 Number of extra gapped extensions for HSPs above 10.0: 0
 Length of query: 942
 Length of database: 765,028,816
 Length adjustment: 140
 Effective length of query: 802
 Effective length of database: 765,028,676
 Effective search space: 613552998152
 Effective search space used: 613552998152
 Neighboring words threshold: 9
 Window for multiple hits: 0
 X1: 16 (7.4 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.9 bits)

S2: 82. (36.2 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3

Filter Align

PRIOR ART

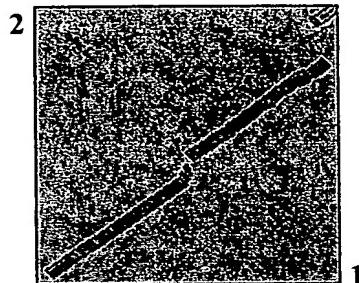
CLAIMED

Sequence 1 lcl|seq_1 Length 918 (1 .. 918)

D/ SEQ ID NO: 2

SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 389 bits (999), Expect = e-106

Identities = 303/949 (31%), Positives = 448/949 (46%), Gaps = 139/949 (14%)

Query: 42 AVLEDAQEQLNDKPLENLWQKLNAATYEVDDILDEYKTATRFF--LQSEYGRYHPKVI- 98
++LE+A+ +++ DK L WL +L Y+ DDILDEY+ A R +S + R VI

Sbjct: 52 SLLEEAKARRMTDKSLVLWLMEALKWAYDADDILDEYEAAAIRLKVTRSTFKRLIDHVI 111

Query: 99 --PFRHKVGKRMQVMKKLNAAEERK-NFHLQEKKIERQAATRE-TGSVLTEPVYGRD 154
P HKV + K+LN + ER+ N E + R T S+LTE + GR

Sbjct: 112 NVPLAHKVA---DIRKRLNGVTLEREELNLAGLEGSQPLDSTKRGVTTSLTESCIVGRA 167

Query: 155 KEKDEIVKILINNVSDAQKLSVLPILGMGGLGKTTLSQMVFNDRVTERFYPKIWICVSD 214
++K+ +--+L+ A + V+PI+G+GG GKTTLSQ++FND+RV E F ++W+CVSD

Sbjct: 168 QDKENLIRLLLEPSDGA--VPVVPIVGLGGAGKTTSQLIFNDKRVEEHFPLRMWVCVSD 225

Query: 215 DFDEKRRIKAIVE-SIEGKSLSDMDLAPLQKKLQELLNGKRYFLVLDLVWNEDQHKWANL 273
DFD KR+ + I E + G+ + L LQ L+E + G + LVLDDVVWNED KW + L

Sbjct: 226 DFDVKRITREITEYATNGRFMDLTNLNMLQVNLKEEIRGTTLLVLDVVWNEDPVWKWESL 285

Query: 274 RAVLKVGASGAFVLTTRLEKVGSIMGTLQPYELSNSLSPEDCWFLFMQRAFGHQ--EEIN 331
A L G G+ V+ TT+ +KV + GT++PY L L+ +D W L +F N

Sbjct: 286 LAPLDAGGRGSVVIVTTQSKKVADVTGTMEPYVLEELTEDDSWSLIESHSFREASCSSTN 345

Query: 332 PNLVAIGKEIVKKCGGVPLAAKTLGGILRFKREEREWEHV-DSPIWNLPQDESSILPALR 390
P + IG++I KK G+P A +G LR K E W V ++ W +P S +L ALR

Sbjct: 346 PRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWREVLETETWEMPPAADVLSALR 405

Query: 391 LSYHHLPLLDQCFVYCAVFPKDTKMAKENLIAFWMAHGFLLSKGNNLELEDV----- 442
SY +LP L CF +CA+F K + K+ LI W+A + S + ED+

Sbjct: 406 RSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQNLIQSTESKRSEDMAEECFDDL 465

Query: 443 -----NEVWNEL-----YLRVSSYSPSLLQK----- 463
N V N+ Y R SP + K

Sbjct: 466 VCRFFFYRYSWGNVVMNDSVHDLARWVSLDEYFRADEDSPHLISKPIRHLSWCSERITNVL 525

Query: 464 -----FXXXXXXXXXXXXQLPSSI 484
LPSS+



Blast Result

Effective length of database: 765,028,676
Effective search space: 595192309928
Effective search space used: 595192309928
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits) **
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 81 (35.8 bits)



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 | Mismatch: -2 | gap open: 5 | gap extension: 2
x_dropoff: 50 expect: 10.000! wordsize: 11 Filter Align

*Prior Art**Claimed**D2**SEQ ID NO: 1***Sequence 1 lcl|seq_1 Length 6658****Sequence 2 lcl|seq_2 Length 4380**

No significant similarity was found



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 | Mismatch: -2 | gap open: 5 | gap extension: 2

x_dropoff: 50 expect: 10.000 wordsize: 11 Filter Align

*Prior Art**Claimed**SEQ ID NO: 3*

D2

Sequence 1 lcl|seq_1 Length 6658

Sequence 2 lcl|seq_2 Length 3660

No significant similarity was found



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 | expect: 10.000 | wordsize: 3 | Filter |

Claimed

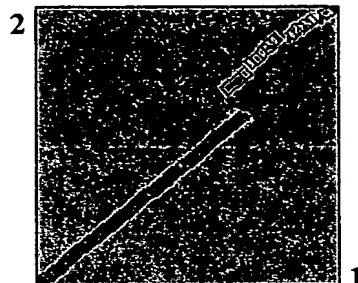
Prev Art

SEQ IDNO: 2

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

D2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 478 bits (1231), Expect = e-133

Identities = 319/896 (35%), Positives = 479/896 (52%), Gaps = 47/896 (5%)

Query: 1 MEIGLAVGG AFLSSALNVLFDR LAPNGD LNMFRXXXXXXXXXXMTLRGIQIVLSDA 60
M L +GG F S + L D+ A N + + R LR I +L A
Sbjct: 1 MSTALVIGGWFAQSFIQTLLDK-ASNCAIQQLARRGLHDDLRLRTSLLR-IHAILDKA 58

Query: 61 ENK-QASNPSVRDWLNELRADVDSAENLIEEVNYEALRLKVEGQHQNFSETSNNQVS--- 116
E + N S+ + + +L+DA AE+L+EE+ Y+A + KVE + S+ + +S
Sbjct: 59 ETRWNHKNTSLVELVRQLKDAAYDAEDLLEELEYQAAKQKVHRGDQISDLFSFSLSTAS 118

Query: 117 -----DDFFLNIKDKLEDTIETLKDLQEIQIGLLGLKE---YFDSTKLETRRPSTSVD 166
DD +++ D+ + + LL + FD + RR ++S
Sbjct: 119 EWLGADGDDAGTRLREIQGKLCNIAADMMDVMQLLAPDDGGRQFDWKVV--RRETSSFLT 176

Query: 167 ESDIFGRQSEIEDLIDRLLSEGASGKKLTVVPIVGMGGQGKTTLAKEYNDERVKNHDL 226
E+ +FGR E E + + LL G+ +V+P+VG+GG GKTTLA+ VYND RV N+F L
Sbjct: 177 ETVVFGRDQEREKVVELLDGSGNSSFSVPLVLVGIGGVGKTTLAQLVYNDNRVGNYFHL 236

Query: 227 KAWYCSEGFDALRITKELLQEIGKFDSKDVKHNNLNQLQVKLKESSLKGKKFLIVLDDVWN 286
K W CVS+ F+ R+TKE++ K + D NL+ LQ LKE + ++FL+VLDDVW+
Sbjct: 237 KVWVCVSDNFNVKRLTKEIIIESATKVEQSD-KLNLDTLQQILKEKIASERFLLVLDDVWS 295

Query: 287 ENYNEWNDLRNIFAQGDIGSKIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLFQRHAF 345
EN ++W L GSK+IVTTR +A ++G ++I + L +A W LF++ AF
Sbjct: 296 ENRDDWERLCAPLRFAARGSKVIVTTRDTKIASIIGTMKEISLDGLQDDAYWELFKCAF 355

Query: 346 ENMDPMGHPELEEVGRQIAAKCKGLPLALKTLAGMLRSKSEVEEWRKIRSEIWELP--H 403
+++P H ELE +GR+IA K KG PLA KTL +LR E W+ I+ SE+W+LP
Sbjct: 356 GSVNPQEHELELEVIGRKIAGKLKGSPLAALKTGSLLRDLVSQEHWRTIMESEVWQLPQAE 415

Query: 404 NDILPALMLSNDLPAHLKRCFSFCAIFPKDYPFRKEQVIHLWIANGLVPVK-DEINQDL 462
N+ILP L LSY LP HL++CF+FCA+F KDY F K ++I WIA G + + ++ +D+
Sbjct: 416 NEILPVWLQSYQHLPGHLRQCFACAVFHKDYLFYKHELIQTWIAEGFIAHQGNKRMEDV 475

Query: 463 GNQYFLELRSRSLSFEKVPNPSKRNIEELFLMHDLVNDLAQCLASSKLCIRLEESQGSHMLE 522
G+ YF EL +RS F+ + ++MHDL++DLAQ S C R+++ +



Lambda K H
0.320 0.137 0.408

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 13,460
Number of extensions: 8847
Number of successful extensions: 46
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 5
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3

Filter

Align

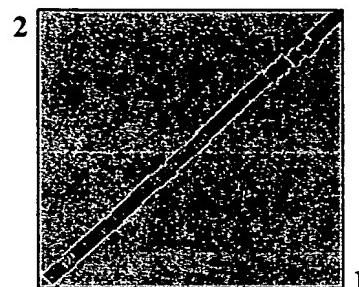
Prior Art

Claimed

D2

SEQ ID NO: 4

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 469 bits (1206), Expect = e-130

Identities = 389/1271 (30%), Positives = 597/1271 (46%), Gaps = 157/1271 (12%)

Query: 49 TLRGIQIVLSDAENKQASNPSVRDWLNELDAVDSAENLIEEVNYEALRLKVEGQHQNF 108

TL +L +A+ ++ ++ S+ WL EL++ A+++++E A+RLKV +

Sbjct: 46 TLLRTHSLLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAAIRLKV-----T 98

Query: 109 ETSNQQVSDDFFLNIK--DKLEDTIETLKDL---QEIQIGLLGLKEYFDSTKLETRRPST 162

++ +++ D +N+ K+ D + L + + +G L + DSTK R +T

Sbjct: 99 RSTFKRLIDHVIINVPLAHKVADIRKRLNGVTLERELNLGALEGSQLDSTK--RGVTT 155

Query: 163 SVDDESDIFGRQSEIEDLIDRLLSEGASGKKLTVVPIVGMGGQGKTTLAKAVYNDERVKN 222

S+ ES I GR + E+LI RLL E + G + VVPIVG+GG GKTTL++ ++ND+RV+

Sbjct: 156 SLLTESCIVGRAQDKENLI-RLLLEPSDGA-VPVPIVGLGGAGKTTLSQLIFNDKRVEE 213

Query: 223 HFDLKAWYCVSEGF DALRITKELLQEIGKFDSKDVHNNLNQLQVKLKE SLKGKKFLIVLD 282

HF L+ W CVS+ FD RIT+E+ + D+ NLN LQV LKE ++G FL+VLD

Sbjct: 214 HFPLRMWVCVSDDFDVKRITREITEYATNGRFMDL-TNLNMLQVNLKEEIRGTTFLVLD 272

Query: 283 DVWNENYNEWNDLRNIFAQGDIGSKIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLFQ 341

DVWNNE+ +W L G GS +IVTT+ VA + G E + L+ + SWSL +

Sbjct: 273 DVWNEDPVWKWESLLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYVLEELTEDDSWSLIE 332

Query: 342 RHAFENMDPMG-HPELEEVGRQIAAKCKGLPLALKTLAGMLRSKSEVEEWKRILRSEIWE 400

H+F +P +EE+GR+IA K GLP + LRSK W+ +L +E WE

Sbjct: 333 SHSFREASCSTNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSIONLQSTESK 392

Query: 401 LPH- -NDILPALMLS YNDLPAHLKRCFSFCAIFPKDYPFRKEQVIHLWIANGLVP-VKDE 457

+P +D+L AL SY++LP LK CF+FCA+F K Y FRK+ +IH+WIA L+ + +

Sbjct: 393 MPPAASDVL SALRRSYDNLPPQLKLCFAFCALFTKGYRFRKD TLIHMWIAQNLIQSTESK 452

Query: 458 INQD LGNQYFLELRSRSLFEKVPNPSKR NIEELFLMHD LVNDLAQ LASSKLCIRLEESQG 517

++D+ + F +L R F R ++M+D V+DLA+ S R +E

Sbjct: 453 RSEDMAEECFDDLVC RFFF-----RYSWGNYVMND SVHDLARW VSLDEYFRADEDSP 504

Query: 518 SHMLEQCRHLSYSIGFN GEFKKLTPLYK-----LEQLRTLLPI -RIEFLHNLS 565

H+ + RHLS+ +++T + + L LRTLL + + EFR ++L

Sbjct: 505 LHISKPIRHLWSWC-----ERITNVLEDNNTGGDAVNPLSSLRTLLFLGQSEFRSYHLL 558
 Query: 566 KRVLHNILPTLRLSRLALSFSQYKIKELPNDLFTKLKLLRFLDISRTWITKLPDSICGLYN 625
 R+ L +R L FS I+ LP+ + LK LR+L +S T I +LP+S+ L
 Sbjct: 559 DRMFR---MLSIRVLDNSNCVIRNLPPSSV-GNLKHLRYLGLSNTRIQRRLPESVTRLCL 613
 Query: 626 LETLLLSSCADLEELPLQMEKLINLRHLDVSNTTLLKMPHLHSRLKSLQVLVGPKFFVD- 684
 L+TLLL C +L LP M +L+ LR L +N + + RL LQ L + VD
 Sbjct: 614 LQTLLLEGCE-ELCRLPRSMSRLVQLRQLK-ANPDVIADIAKVGRILIELQELKA--YNVDK 669
 Query: 685 --GWRMEDLGEAQNLHGSLSVVKLENVVDRREAVKAKMREKNHVEQLSLEWSESSIADNS 742
 G + +L LHG LS+ L+NV RE+ KA++ EK ++ L L W++ A
 Sbjct: 670 KKKGHGIAELSAMNQLHGDSLIRNLQNVEKTRESRKARLDEKQKLKLLDLRWADGRGAGEC 729
 Query: 743 QTESDILDELCPHKNIKKVEISGYRGTNFPNWADPLFLKLVNLNLSRNCKDCYSLPALGQ 802
 + +L L PH N+++ I Y GT+ P+W+ D + + LR+C LP LGQ
 Sbjct: 730 DRDRKVLKGLRPHPNLRELSIKYYGGTSSPSWMTDQYLPNMETIRLRSARLTELPCLGQ 789
 Query: 803 LPCLKFLSVKGGMHIGIRVVTEEFYGRLLSSKKPFNSLEKLEFEDMTEWKQWH--ALGIGEFP 860
 L L+ L + GM +R + +FYG F LE L M + +W FP
 Sbjct: 790 LHILRHLHIDGMSQVRQINLQFYG-TGEVSGFPLLELLNIRRMPSELLEWSEPRRNCCYFP 848
 Query: 861 TLENLSIKNCPELSLEIPIQFSSLKRLEVSDCPVFDDAQLFRSQLEAMKQIEEIDICDC 920
 L L I++CP L +P +L+ L +S +V + + + + +C
 Sbjct: 849 RLHKLLIEDCPRLR-NLPSLPPTLEELRISRTGLVDPFGHNGDVTNVSLSSLHVSEC 907
 Query: 921 NSVTSFPFSILPTTLKRIQISRCPKLKLEAPVGEMFVEYLRVNDCGCVDDISPEFLPTA- 979
 + S +L L ++ + DC ++ + E TA
 Sbjct: 908 RELRSLSEGLLQHNLVALKTA-----AFTDCDSLEFLPAEGFRTAI 948
 Query: 980 --RQLSIENCQNVTRFLIPTATETLRISNC----ENVEKLSVACGGAAQMITSNLIWGXXX 1033
 L + NC FL+P++ E L++ C N + LS ++ L+I
 Sbjct: 949 SLESLIMITNCPLPCSFLLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSLSFLDI---- 1003
 Query: 1034 XXXXXXXXXXXXXXXXXDCPEIEGELPFNLEILRIIYCKKLVNGRKEWHLQRLTELWIDH 1093
 DCP + P L L + LVN QRL +
 Sbjct: 1004 -----KDCPNLSSFPPLCQLSALQHLSLVN-----CQRLQSI---- 1037
 Query: 1094 DGSDEDIEHWELPCSIQRLTIKNLKTLSSQHL-----KSLSLQYLCI-----EG 1138
 ++ S++ LTI+N L+ H S T L + +G
 Sbjct: 1038 -----GFQALTSLESLTIQNCPRLTMSHSLVEVNNSDTGLAFNITRWMRRTGDDG 1089
 Query: 1139 YL---XXXXXXXXXXXXHLSLQTLQIWN----FLNXXXXXXXXXXXXIDDGP 1190
 + HLT LQ L+I I DCP
 Sbjct: 1090 LMLRHRAQNDSSFGLLQHLTFLQFLKICQCPQLVFTGEEEKWRNLTSLQILHIVDCP 1149
 Query: 1191 NLQLSFESALPS--SLSQLFIQDCPNLQSLPKGMPSLSSKLSIFNCPLLTPLLEFDKGE 1248
 NL+ L + L S SLS L+I CP + + P G+ SL+ L I CP L + G+
 Sbjct: 1150 NLEVL-PANLQSLCSLSTLYIVRCPRIHAFFPGGVMSLAHLVIHECPQLCQRCDPGGD 1208
 Query: 1249 YWPQIAHIPIII 1259
 WP IA++P I
 Sbjct: 1209 DWPLIANVPRI 1219

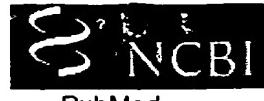
CPU time: 0.09 user secs. 0.01 sys. secs. 0.10 total secs.

Lambda	K	H
0.320	0.137	0.408

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 10,906

Number of extensions: 7195
Number of successful extensions: 35
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter Align

DovArt

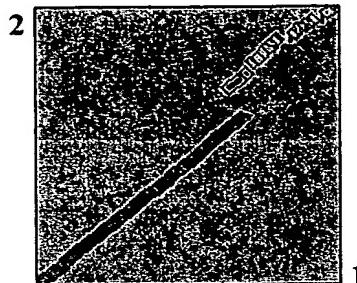
Clarend

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

DB

Seq(ON)2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 478 bits (1231), Expect = e-133

Identities = 319/896 (35%), Positives = 479/896 (52%), Gaps = 47/896 (5%)

Query: 1 MEIGLAVGGAFLSSALNVLFDR LAPNGD LNMFRXXXXXXXXXXMTL RG I QIVL SDA 60
M L +GG F S + L D+ A N + + R LR I +L A

Sbjct: 1 MSTALVIGGWFAQSFIQTL LDK-ASNCAIQQLARRGLHDDLRLRTSLLR-I HAILDKA 58

Query: 61 ENK-QASNPSVRDWLNE RD AVDSAENLIEEVNYEALRLKVE GHQNF SETSNQQVS--- 116
E + N S+ + + +L+DA AE+L+EE+ Y+A + KVE + S+ + +S

Sbjct: 59 ETRWNHKNTSLVELVRQLKDAAYDAEDLLEELEYQA AKQKV EHR GDQISDLFSF SLSTAS 118

Query: 117 -----DDFFLNIKDKLEDTIETLKD LQE QIG LLG LKE -- YFD STKLETRRPSTS VDD 166
DD +++ D+ + + LL + FD + RR ++S

Sbjct: 119 EWLGADGDDAGTRLREI QGKLCNIAADMMDVMQL LAP DDG GRQFDW KV -- RRET SSFLT 176

Query: 167 ESDIFGRQSEIEDLIDRLLSEGASGKKLTVVPIVGMGGQGKTTLAKAVYNDERVKNHFDL 226
E+ +FGR E E +++ LL G+ +V+P+VG+GG GKTTLA+ VYND RV N+F L

Sbjct: 177 ETVVFG RDQEREK VVELL DSGSGN SFSV LPLVGIGGVGKTTLAQLVYNDNRVG NYFHL 236

Query: 227 KAWYC VSEGFD ALRITKELLQ EIGKFDSK DVHN NLNQLQVKL KESLKGKKFLIVLDDVWN 286
K W CVS+ F+ R+TKE++ K + D NL+ LQ LKE + ++FL+VLDDVW+

Sbjct: 237 KVWVCVSDNF NVKRLTKEII ESATKVEQSD-KLNLDL TLQ QILKE KIASERFLL VLDDVWS 295

Query: 287 ENYNEWNDLRNIFAQGDIGSKIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLFQRHAF 345
EN ++W L GSK+IVTTR +A ++G ++I + L +A W LF++ AF

Sbjct: 296 ENRDDWERLCAPLRFAARGSKVIVTTRDTKIASIIGTMKEISLDGLQDDAYWELFKCAF 355

Query: 346 ENMDPMGH P ELEEVGRQIAAKCKGLPLALKTLAGMLRSKSEVEEWKRILRSEI WELP--H 403
+++P H ELE +GR+IA K KG PLA KTL +LR E W+ I+ SE+W+LP

Sbjct: 356 GSVNPQEHLELEVIGRKIA GKLKGSP LAAKTLGSLL RDVS QEH WRTIMESEVW QLPQAE 415

Query: 404 NDILPALMLS YNDLPAHLKRCFS FCA IFPKD YPFRKEQVIHLWIANGL VPVK-DEINQDL 462
N+ILP L LSY LP HL+ +CF+FCA+F KDY F K ++I WIA G + + ++ +D+

Sbjct: 416 NEILPV LWL S YQHLP GHL RQCF A VFKHDYL FYKHELI QTWIAEGFIAHQGNKRMEDV 475

Query: 463 GNQYF LE LRSRSL F EKVPNPSKR NIEELFLMHD LVNDLAQ LASS KLCIRLE E S QGSHMLE 522
G+ YF EL +RS F+ + ++MHDL++DLAQ S C R+++ +

Sbjct: 476 GSSYFHELVNRSFFQ-----ESRWRGRYVMHDLIHDLAQFISVGECRIDDKSKEPS 529

Query: 523 QCRHLSYSIGFNGEFKKLTPLYKLEQLRTLLPIRIEFLRNHLNSK---RVLHNILPTLRS 578
RHLS ++ E KL +LRTL+ + ++K + H++ L+

Sbjct: 530 TTRHLSVAL---TEQMKLVDGSGYNKLRTLMINNQRNQYPYMTKVNSCLLPHSLFKRLKR 586

Query: 579 LRALSFSQYKIKELPNLFTKLKLLRFLDIS-RTWITKLPDSICGLYNLETLLLSSCADL 637
+ L + +KELP D+ L LR+LDIS I +LP+S+C LYNL+ L L C L

Sbjct: 587 IHVVLVLQKCGMKELP-DIIGDLIQLRYLDISYNACIQLPESLCDLYNLQALRLWGC-QL 644

Query: 638 EELPLQMEKLIINLRHLDVSNTRRLKMPHLHSRLKSLQVLVGPFFVD-GWRMEDLGEAQN 696
P M KLINLR L V + K+ + +L SLQ L K + G ++ +L

Sbjct: 645 RSFPQGMSKLIINLRQLRVEDEIISKI-YEVGKLISLQELSAFKVLNNHGNKLAELSGLTQ 703

Query: 697 LHGSLSVVVKLENVVDRREAVKAKMREKNHVEQLSLEWSE--SSIADNSQTESDILDEL 753
L +L + LENV + EA KAK+ K ++E L LEW+ SS+ ++L L

Sbjct: 704 LRSTLRITNLENVGSKKEASKAKLHRKQYLEALEWAAGQVSSLEHELLVSEEVLLGLQ 763

Query: 754 PHKNIKKVEISGYRGTFNFPNWADPLFLKLVNLSLRNCKDCYSLPALGQLPCLKFLSVKG 813
PH +K + I GY G P+W+ + L L L NC L +GQLP LK L +K

Sbjct: 764 PHHFLKSLSLTIRGSGATVPSWLDVKMLPNLGTALKLENCTRLEGLSYIGQLPHLKVLHMKR 823

Query: 814 MHGIRVVTEEFYGRLLSSKKPFNSLEKLEFEDMTEWKQWHALGIGEFPTLENLSIKN 869
M ++ ++ E G SK F LE+L EDM K++ + + P L+ + +KN

Sbjct: 824 MPVVKQMSHELCGCTKSKL-FPRLEELVLEDMPTLKEFP--NLAQLPCLKIIHMKN 876

Score = 79.3 bits (194), Expect = 1e-12

Identities = 124/517 (23%), Positives = 191/517 (35%), Gaps = 142/517 (27%)



Query: 780 FLKLVNLSLRNCKDCYSLPALGQLPCLKFLSVKGMHGIRVVTEEFYGRLLSSKKPFNSLEK 839
F +L L ++ L +L +LPCLK +KG+ ++ + + + + F LE

Sbjct: 997 FPRLEELIEIKGMLTFEELHSLEKLPCLKVFRIKGLPAVKKIGHGLFDSTCQRECFFPRLED 1056

Query: 840 LEFEDMTEWKQWHALGIGE-FPTLENLSIKNCPELSLEIPIQFS----- 882
L DM W++W E F L L I+ CP+L +PI S

Sbjct: 1057 LVLSDMPAWEWSWAEREELFSCLCRLKIEQCPKLKCLLPIPHSLIKLELWQVGLTGLPG 1116

Query: 883 -----SLKRLEVSDCPVVFDDAQLFRSQLREAMKQIEIIDCDCNSVTSFPF 928
SL L + CP ++ + S + I I I +C + P

Sbjct: 1117 LCKGIGGGSSRTASLSLLHIKCPNLRNLGEGLLS--NHLPHINAIRIWECAELLWLPV 1174

Query: 929 SILP--TTLKRIQISRCPKLKLEAPVGE-----MFVEYLRVNDCGCVDDISP---EFLP 977
TTL+ + I CPKL E ++ L + DCG + P L

Sbjct: 1175 KRFREFTTLENLSIRNCPKLMSMTQCENDLLLPLLIKALELGDCGNLGKSLPGCLHNLS 1234

Query: 978 TARQLSIENCQ--NVTRFLIPTATE--TLRISNCENVEKLSVACGAAQMITSNIWGXX 1032
+ QL+I NC ++ R ++ E T+RI NC+ +

Sbjct: 1235 SLTQLAISNCPYMVS LPREVMLHLKELGTVRIENC DGL----- 1272

Query: 1033 XXXXXXXXXXXXXXXXDCPEIEG-ELPFNLEILRIIYCKKLV--NGRKEWHLQRLTEL 1089
IEG ++ +L+ L II C +L+ G ++ + L EL

Sbjct: 1273 -----GSIEGLQVLKSLKRLAIIGCPRLLNNEGDEQGEVLSLLEL 1312

Query: 1090 WIDHDGSDDEDIEHWELPCSIQRLTIKNLKTLSSQH-LKSLTLSQYLCIEGYLXXXXXXX 1148
+D ++ IKN TL H L+ + S Q + +

Sbjct: 1313 SVDK-----TALLKLSLIKNTLPFIHSLRIIWSPQKVMFD-----LEE 1350

Query: 1149 XXXXXHHTLSLQTLQIWNFLNXXXXXXXXXXXXIDDCPNLQSL-FESALPSSLSQL 1207
LT+L+ L+ + C NLQSL E SL L

Sbjct: 1351 QELVHSLTALRRLEFFR-----CKNLQSLPTELHTLPSLHAL 1387

Query: 1208 FIQDCPNLQSLPFPKGMPSSLSKLSIFNC-PLLTPLL 1243
+ DCP +QSLP KG+P+ L+ L +C P+LT LE

Sbjct: 1388 VVSDCPQIQSLPEKGLPTLLTDLGFHDCHPVLT AQL 1424

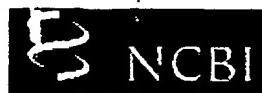
CPU time: 0.20 user secs. 0.01 sys. secs 0.21 total secs.

Lambda K H
0.320 0.137 0.408

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 13,460
Number of extensions: 8847
Number of successful extensions: 46
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 5
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)





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Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3

 Filter

Prior Art

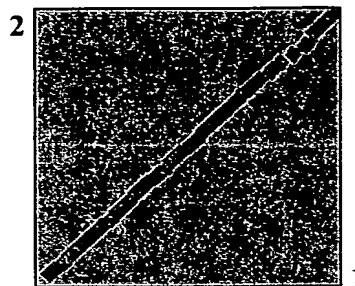
Claimed

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

D3

Seq ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 469 bits (1206), Expect = e-130

Identities = 389/1271 (30%), Positives = 597/1271 (46%), Gaps = 157/1271 (12%)

Query: 49 TLRGIQIVLSDAENKQASNPSVRDWLNELRAVDSAENLIEEVNYEALRLKVEGQHQNF 108

TL +L +A+ ++ S+ WL EL++ A+++++E A+RLKV +

Sbjct: 46 TLLRTHSLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAAIRLK V-----T 98

Query: 109 ETSNQQVSDDFFLNIK--DKLEDTIETLKDL---QEIQIGLLGLKEYFDSTKLETRRPST 162

++ +++ D +N+ K+ D + L + + G L + DSTK R +T

Sbjct: 99 RSTFKRLIDHVIINVPLAHKVADIRKRLNGVTLERELNLGALEGSQPLDSTK---RGVTT 155

Query: 163 SVDDESDIFGRQSEIEDLIDRLLSEGASGKKLTVVPIVGMGGQGKTTLAKAVYNDERVKN 222

S+ ES I GR + E+LI RLL E + G + VVPIVG+GG GKTTL++ ++ND+RV+

Sbjct: 156 SLLTESCIVGRAQDKENLI-RLLLEPSDGA-VPVVPIVGLGGAGKTSQLIFNDKRVEE 213

Query: 223 HFDLKAWYCVSEGFDALRITKELLQEIGKFDSKDVHNLLNQLQVKLKESSLKGKKFLIVLD 282

HF L+ W CVS+ FD RIT+E+ + D+ NLN LQV LKE ++G FL+VLD

Sbjct: 214 HFPLRMWVCVSDDFDVKRITREITEYATNGRFMDL-TNLNMLQVNLKEEIRGTTFLLVLD 272

Query: 283 DVWNENYNEWNDLRNIFAQGDIGSKIIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLFQ 341

DVWNE+ +W L G GS +IVTT+ VA + G E + L+ + SWSL +

Sbjct: 273 DVWNEDPVWKESLLAPLDAGGRGSVVIVTTQSKKVADVTGTMEPYVLEELTEDDSWSLIE 332

Query: 342 RHAFENMDPMG-HPELEEVGRQIAAKCKGLPLALKTLAGMLRSKSEVEEWKRILRSEIWE 400

H+F +P +EE+GR+IA K GLP + LRSK W+ +L +E WE

Sbjct: 333 SHSFREASCSTSNNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSIONREVLETETWE 392

Query: 401 LPH--NDILPALMLSNDLPAHLKRCFSFCAIFPKDYPFRKEQVIHLWIANGLVP-VKDE 457

+P +D+L AL SY++LP LK CF+FCA+F K Y FRK+ +IH+WIA L+ + +

Sbjct: 393 MPPAASDVLSALRRSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQNLIQSTESK 452

Query: 458 INQD LGNQYFLELRSRSLFEKVPNPSKRNIEELFLMHDLVNDLAQLASSKLCIRLEESQG 517

++D+ + F +L R F R ++M+D V+DLA+ S R +E

Sbjct: 453 RSEDMAEECFDDLVCRFFF-----RYSWGNYVMNDSVHDLARWVSLDEYFRADEDSP 504

Query: 518 SHMLEQCRHLSYSIGFNGEFKKLTPLYK-----LEQLRTLLPI-RIEFLRHNL 565

H+ + RHLS+ +++T + + L LRTLL + + EFR ++L

Blast Result

Sbjct: 505 LHSKPIRHLSWCS-----ERITNVLEDNNNTGGDAVNPLSSLRTLLFLGQSEFRSYHLL 558
 Query: 566 KRVLNILPTLRLSRLALSFSQYKIKELPNDLFTKLKLLRFLDISRTWITKLPDSICGLYN 625
 R+ L +R L FS I+ LP+ + LK LR+L +S T I +LP+S+ L
 Sbjct: 559 DRMFR----MLSIRVLDFSNCVIRNLPPSSV-GNLKHLRYLGLSNTRIQRLPESVTRLCL 613
 Query: 626 LETLLLSSCADLEELPLQMEKLINLRHLDVSNTRRLKMLHLSRLKSLQVLVGPFFVD- 684
 L+TLLL C +L LP M +L+ LR L +N + + RL LQ L + VD
 Sbjct: 614 LQTLLLEGCA-ELCRLPRSMSRLVKLRQLK-ANPDVIADIAKVGR利ELQELKA--YNVDK 669
 Query: 685 --GWRMEDLGAEAQNLHGSLSVVKLENVDRREAVKAKMREKNHVEQLSLEWSSESSIADNS 742
 G + +L LHG LS+ L+NV RE+ KA++ EK ++ L L W++ A
 Sbjct: 670 KKKGHIAELSAMNQLHGDSLIRNLQNVEKTRESRKARLDEKQKLKLLDLRWADGRGAGEC 729
 Query: 743 QTESDILDELCPHKNIKKVEISGYRGTFNFPNWADPLFLKLVNLSLRNCKDCYSLPALGQ 802
 + +L L PH N++++ I Y GT+ P+W+ D + + LR+C LP LGQ
 Sbjct: 730 DRDRKVVLKGLRPHPNLRELSIKYGGTSSPSWMTDQYLPNMETIRLRCARLTELPCLGQ 789
 Query: 803 LPCLKFLSVKGHMIGIRVVTEEFYGRLLSSKKPFNSLEKLEFEDMTEWKQWH--ALGIGEFP 860
 L L+ L + GM +R + +FYGF LE L M + +W FP
 Sbjct: 790 LHILRHLHIDGMSQVRQINLQFYG-TGEVSGFPLLELLNIRRMPSELWSEPRRNCCYFP 848
 Query: 861 TLENLSIKNCPELSLEIPIQFSSLKRLEVSDCPVFDDAQLFRSQLEAMKQIEEIDICDC 920
 L L I++CP L +P +L+ L +S +V + + + + +C
 Sbjct: 849 RLHKLLIEDCPRLR-NLPSLPPTEELRISRTGLVDPFGHNGDVTTNVSLSSLHVSEC 907
 Query: 921 NSVTSPPFSILPTTLKRIQISRCPKLKLEAPVGEMFVEYLRVNDCGCVDDISPEFLPTA- 979
 + S +L L ++ + DC ++ + E TA
 Sbjct: 908 RELRSLSSEGLLQHNLVALKTA-----AFTDCDSLEFLPAEGFRTAI 948
 Query: 980 --RQLSIENCQNVTRFIPTATETLRISNC---ENVEKLSVACGGAAQMITSNIWGXXX 1033
 L + NC FL+P++ E L++ C N + LS ++ L+I
 Sbjct: 949 SLESLIMITNCPLPCSFLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSLSFLDI---- 1003
 Query: 1034 XXXXXXXXXXXXXXXXXDCPEIEGELPFNLEILRIIYCKKLVNGRKEWHLQRLTELWIDH 1093
 DCP + P L L + LVN QRL +
 Sbjct: 1004 -----KDCPNLSSFPFPGLCQLSALQHLSLVN-----CQRLQSI---- 1037
 Query: 1094 DGSDEDIEHWELPCSIIQRLTIKNLKTLSSQHL----KSLTLSQYLCI-----EG 1138
 ++ S++ LTI+N L+ H S T L + +G
 Sbjct: 1038 -----GFQALTSLESLTIQNCPRLTMSHLVEVNNSSDTGLAFNITRWMRRRTGDDG 1089
 Query: 1139 YL---XXXXXXXXXXXXHLSLQTLQIWN----FLNXXXXXXXXXXXXXIDDCP 1190
 + HLT LQ L+I I DCP
 Sbjct: 1090 LMLRHRAQNDSSFGGLLQHLTFLQFLKICQCPQLVTFTGEEEKWRNLTSLQILHIVDCP 1149
 Query: 1191 NLQSLFESALPS--SLSQLFIQDCPNLQSLPFKGMPSSLSKLSIFNCPLLTPLEFDKGE 1248
 NL+ L + L S SLS L+I CP + + P G+ SL+ L I CP L + G+
 Sbjct: 1150 NLEVL-PANLQSLCSLSTLYIVRCPRIHAFFPGGVMSLAHLVIHECPQLCQRCDDPGGD 1208
 Query: 1249 YWPQIAHIPIII 1259
 WP IA++P I
 Sbjct: 1209 DWPLIANVPRI 1219

CPU time: 0.08 user secs. 0.02 sys. secs 0.10 total secs.

Lambda K H
0.320 0.137 0.408

Gapped Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 10,906

Number of extensions: 7195
Number of successful extensions: 35
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



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Matrix BLOSUM62 gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter Align

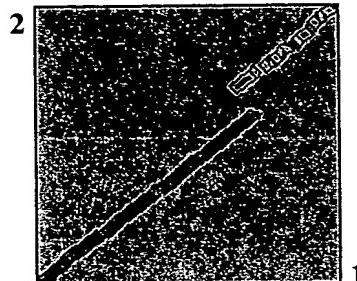
*Prior Art**Claimed*

Sequence 1 lcl|seq_1 Length 1220 (1 .. 1220)

D4

Seq IDN:2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 401 bits (1031), Expect = e-109
Identities = 300/911 (32%), Positives = 463/911 (49%), Gaps = 69/911 (7%)

Query: 1 MEIGLAIGGAFLSSALNVLFDR LAPNGD LLMFRKHTDD VELFEKLG DILL S LQIVL SDA 60
M L IGG F S + L D+ A N + + R+ +L +L LL + +L A
Sbjct: 1 MSTALVIGGWFAQSFI QTLLDK-ASNCAIQQLARRGLHDDL-RRLRTSLLRIHAILDKA 58

Query: 61 ENK-KASNQFVSQLWHLKLQTAVDAAENLIEQVN YEA RLKVET SNQVSDL---NLCLSD 116
E + N + + + +L+ A AE+L+E++ Y+A + KVE Q+SDL +L +
Sbjct: 59 ETRWNHKNTSLVELVRQLKDAAYDAEDLLEELEYQAAKQKVEHRGDQISDLFSFSLSTAS 118

Query: 117 DFF-----LNIKKKL---EDTIKKLEVLEKQIGRGLKEHFISTKQET RTPST 161
++ I+ KL D + +++L G G + + ++ET +
Sbjct: 119 EWLGADGDDAGTRLREIQGKLCNIAADMMDVMQLLAPDDG--GRQFDWKVVRRET---S 172

Query: 162 SLVDDSGIFGRKNEIENLVGRLLSM DT KRN LAVVPIVGMGGMGKTT LAKAVYND ERVQK 221
S + ++ +FGR E E +V LL + + +V+P+VG+GG+GKTT LA+ VYND RV
Sbjct: 173 SFLTETVVFG RDQEREK VVELL DSGSGN SSFSV LPLVGIGGVGKTT LAQ LVY NDNR VGN 232

Query: 222 HFGLTA WFCVSEAYDAFRITKGLLQEIGSTD LKADDNLNQLQVKLKADDNLNQLQVKLKE 281
+F L W CVS+ ++ R+TK ++ +T ++ D LN L+ LQ LKE
Sbjct: 233 YFHLKVVVCVSDNFNVKRLTKEIIES-ATKVEQSDKLN-----LDTLQQILKE 279

Query: 282 KLN GKRFLVVL DDWNDN PWE DLLRN LFLQGDIGSKII VTTRKESVAL MMD S-GAIYMG 340
K+ +RFL+V LDDV W++N +W+ L GSK+IVTTR +A ++ + I +
Sbjct: 280 KIASERFLLV LDDV WSEN RDDW ERLCAP LRFA ARG SKVIV TTD KIASI IGT MKE IS LD 339

Query: 341 ILSSED SWAL FKRHS LEHKDP KEH PEFEEV GKQIAD XXXXXXXXXXXX RSKSEVDE 400
L + W LFK+ + +P+EH E E +G++IA R +
Sbjct: 340 GLQDDAYWELFKCAF GSVP NQEH LELEV IGRKIAGKLKG SPLA AKTLGSLL RLDV SQ EH 399

Query: 401 WRN ILRSEI WELPSCS NGILPAL MLYNDLPAHLKQCFAY CAIYPKDYQFRKEQVIHLWI 460
WR I+ SE+W+LP N ILP L LSY LP HL+QCFA+CA++ KDY F K ++I WI
Sbjct: 400 WRTIMESEVWQLPQAENEILPVLWLSYQHLP GHLRQCFACVFHKDYL FYKHELI QT WI 459

Query: 461 ANGLV-HQFHS----GNQYFIELRSRSLFEMASEP SERDVEEFLMHDLVNDLAQIASSN 514
A G + HQ + G+ YF EL +RS F+ R ++MHDL++DLAQ S

Sbjct: 460 AEGFIAHQGNKRMEDVGSSYFHELVNRSFFQ----ESWRGRYVMHDLIHDLAQFISVG 514

Query: 515 HCIRLEDNKGSMLEQCRHMSYSIGQDGEFEKLKSLFKSEQLRTLLPID--IQFHYSKKL 572
C R++D+K RH+S ++ E KL +LRTL+ + Q+ Y K+

Sbjct: 515 ECHRIIDDKSKETPSTTRHLSVAL---TEQMKLVDGSGYNKLRTLMINNQRNQYPYMTKV 571

Query: 573 SKRVL-HNILPTLRLSRLALSLSHYQIEVLPNDLFIKLKLLRFLDLS-ETSITKLPSIFV 630
+ +L H++ L+ + L L ++ LP D+ L LR+LD+S I +LP+S+

Sbjct: 572 NSCLLPHSLFKRLKRIHVVLVLQKCGMKELP-DIIGDLIQLRYLDISYNACIQRLPESLCD 630

Query: 631 LYNNXXXXXXXXXXXXXXQMEKLINLRHLDISNTRRLKMPHLHSRLKSLQVLVGAKFL 690
LYN M KLINLR L + + K+ + +L SLQ L K L

Sbjct: 631 LYNLQALRLWGCQLRSFPQG-MSKLINLRQLRVEDEIISKI-YEVGKLISLQELSAFKVL 688

Query: 691 VG-GWRMEYLGEAHNLYGSLSILELENVDRREAVKAKMREKNHVEQLSLEWSE--SIS 746
G ++ L L +L I LENV + EA KAK+ K ++E L LEW+ S

Sbjct: 689 NNHGNKLAELSGLTQLRSTLRITNLENGSKEEASKAKLHRKQYLEALELEWAAGQVSSL 748

Query: 747 ADNSQTERDILDELPHKNIKAVEITGYRGTFNPNWADPLFVKLVHLYLRNCKDCYSLP 806
++L L+PH +K++ I GY G P+W+ + L L L NC L

Sbjct: 749 EHLLVSEEVLLGLQPHHFLKSLTIRGSGATVPSWLDVKMLPNLGTLCLENCTRLEGLS 808

Query: 807 ALGQLPCLEFLSIRGMHGIRVVTEEFYGRLLSSKKPFNSLVKLRFEDMPEWKQWHTLGIGE 866
+GQLP L+ L ++ M ++ ++ E G SK F L +L EDMP K++ L +

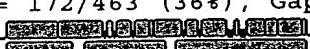
Sbjct: 809 YIGQLPHLKVLHMKRMPVVKQMSHELCGCTKSKL-FPRLEELVLEDMPNLKEFPNL--AQ 865

Query: 867 FPTLEKLSIKN 877
P L+ + +KN

Sbjct: 866 LPCLKIIHMKN 876

Score = 71.6 bits (174), Expect = 2e-10

Identities = 110/463 (23%), Positives = 172/463 (36%), Gaps = 88/463 (19%)



Query: 788 FVKLVHLYLRNCKDCYSLPALGQLPCLEFLSIRGMHGIRVVTEEFYGRLLSSKKPFNSLVK 847
F +L L ++ L +L +LPCL+ I+G+ ++ + + ++ F L

Sbjct: 997 FPRLEELIKEMLTFEELHSLEKLPCLKVFRIKGLPAVKKIGHGLFDSTCQRECFCPRLED 1056

Query: 848 LRFEDMPEWKQWHTLGIGE-FPTLEKLSIKNCPELSLEIPIQFSSLKRLDICDCSVTSF 906
L DMP W++W E F L +L I+ CP+L +PI

Sbjct: 1057 LVLSDMPAWEWEWSWAEREELFSCLCRLKIEQCPKLKCLLPI----- 1097

Query: 907 PFSILPTTLKRIKISGCPKLKLEAPVGE---MFVEYLSVIDC---GCVDDISPEFLPT 958
P S++ L ++ ++G P L G + L +I C + + + LP

Sbjct: 1098 PHSLIKLELWQVGLTGLPGLCKGIGGGSSRTASLSLLHIICKPNLRNLGEGLLSNHLPH 1157

Query: 959 ARQLSIENCHN----VTRFLIPTATESLHIRNCEKL-SMA-CGGAAQLTLSNIWGXXXX 1011
+ I C V RF T E+L IRNC KL SM C L I

Sbjct: 1158 INAIRIWECAELLWLPVKRFREFTTLENLSIRNCPKLMSMTQCEENDLLLPLLIKALELG 1217

Query: 1012 XXXXXXXXXXXXXXXTYCPEIEGELP----FNLQILDIFYCKKLVNGRKE--WHLQRL 1063
C + LP +L L I C +V+ +E HL+ L

Sbjct: 1218 D-----CGNLGKSLPGCLHNLSSLTQLAISNCPYMVSLSPREVMLHLKEL 1261

Query: 1064 TELWIKHGSDEHIEHWELPSSIQRRLFIFNL-----KTLSSQHL----- 1102
+ I++ IE ++ S++RL I + LS L

Sbjct: 1262 GTVRIENCGLGSIEGLQVLKSLKRLAIIGCPRLLLNEGDEQGEVLSLLELSVDKTALLK 1321

Query: 1103 ----KSLTLSQFLRIVGNXXXXXXXXXH-LTSLQTLQIWNFLNXXXX-XXXXXX 1155
+L + LRI+ + H LT+L+ L+ + N

Sbjct: 1322 LSLIKNTLPFIHSLRIIWSPQKVMFDLEEQELVHSLTALRRLEFFRCKNLQSLPTELHTL 1381

Query: 1156 XXXXXXIIISNCNLQSLPLKGMPSSLSTLSISKC-PLLTPLLE 1197
++S+CP +QSLP KG+P+ L+ L C P+LT LE

Sbjct: 1382 PSLHALVVSDCPQIQSLPEKGLPTLTDLGFHDHCHPVLTAQLE 1424

CPU time: 0.16 user secs. 0.00 sys. secs. 0.16 total secs.

Lambda K H
0.320 0.137 0.406

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 12,261
Number of extensions: 8166
Number of successful extensions: 28
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 3
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1220
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1078
Effective length of database: 765,046,036
Effective search space: 824719626808
Effective search space used: 824719626808
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter Align

Prior Art

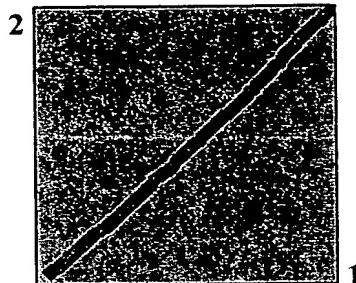
Claimed

Seq ID: 4

Sequence 1 lcl|seq_1 Length 1220 (1 .. 1220)

D4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 399 bits (1024), Expect = e-109
 Identities = 352/1233 (28%), Positives = 552/1233 (44%), Gaps = 129/1233 (10%)

```

Query: 50 LLSLQIVLSDAENKKASNQFVSQWLHKLQTAVDAEENLIEQVNYEALRLKVETSNQQVSD 109
       LL +L +A+ ++ +++ + WL +L+ A++++++ A+RLKV S +
Sbjct: 47 LLRTHSLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAIRLKVRSTFKR-- 104

Query: 110 LNLCLSDDFFLNIK--KKLEDTIKKLE--VLEKQIGRLGLKEHFISTKQETRTPSTSVD 165
       L D +N+ K+ D K+L LE+++ LG E R +TSL+
Sbjct: 105 ---LIDHVIINVPLAHKVADIRKRLNGVTLERELEN-LGALEGSQPLDSTKRGVTTSLT 159

Query: 166 DSGIFGRKNEIENLVGRLLSMDTKRKNLAVVPIVGMMGGKTTLAKAVYNDERVQKHGGL 225
       +S I GR + ENL+ LL + + VVPIVG+GG GKTTL++ ++ND+RV++HF L
Sbjct: 160 ESCIVGRAQDKENLIRLLL--EPSDGAVPVVPPIVGLGGAGKTTLSQLIFNDKRVEEHFPL 217

Query: 226 TAWFCVSEAYDAFRITKGLLQEIGSTDLKADDNLNQLQVKLKADDNLNQLQVKLKEKLNG 285
       W CVS+ +D RIT+ + T+ + L NLN LQV LKE++ G
Sbjct: 218 RMWVCVSDDFDVKRITREI-----TEYATNGRFMDLT-----NLNMLQVNLCHEIRG 264

Query: 286 KRFLVVLDDVVWNNDNYPEWDDLRNLFLQGDIGSKIIVTTRKESVALMMDGAIY-MGILSS 344
       FL+VLDDVVNN++ +W+ L G GS +IVTT+ + VA + + Y + L+
Sbjct: 265 TTFLVVLDDVVWNEDPVWKESLLAPLDAGGRGSVVIVTTQSKKADVGTMEPYVLEELTE 324

Query: 345 EDSWALFKRHS-EHKDPKEHPEFEVGKQIADXXXXXXXXXXXXXXRSKSEVDEWRN 403
       +DSW+L + HS E +P EE+G++IA RSK WR
Sbjct: 325 DDSWSLIESHSFREASCSSNTPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWRE 384

Query: 404 ILRSEIWELPSCSNGILPALMLSNDLPAHLKQCFAYCAIYPKDYQFRKEQVIHLWIANG 463
       +L +E WE+P ++ +L AL SY++LP LK CFA+CA++ K Y+FRK+ +IH+WIA
Sbjct: 385 VLETETWEMPPAASDVLSALRRSYDNLPPQLKLCFAFCALFTKGYFRKDTLIHMWIAQN 444

Query: 464 LVHQFHS-----GNQYFIELDRSRSLFEMASEP SERDVEEFLMHDLVNDLAQIASSNHC 517
       L+ S + F +L R F + + +M+D V+DLA+ S +
Sbjct: 445 LIQSTESTKRSEDMAEECFDDLVCRFFFYSWG-----NYVMNDSVHDLARWVSLDEYF 497

Query: 518 RLEDNKGSshmleqcrhmsysigqdgefeklkslfkseq-----LRTLLPIDIQF 566
       R +++ H+ + RH+S+ E++ ++ + LRTLL +
  
```


Blast Result

Sbjct: 498 RADEDSPHLISKPIRHLWSWC-----ERITNVLEDNNNTGGDAVNPLSSLRTLLFLG--- 548

Query: 567 HYSKKLSKRVLHNILPTLRLSRLALSLSHYQIEVLPNDLFIKLKLLRFLDLSETSITKLPD 626
 S+ S +L + L +R L S+ I LP+ + LK LR+L LS T I +LP+

Sbjct: 549 -QSEFRSYHLLDRMFRMLSIRVLDFSNCVIRNLPSVG-NLKHLRYLGLSNTRIQRLPE 606

Query: 627 SIFVLYNXXXXXXXXXXXXXXQMEKLINLRHL-----DISNTRRLKMPHLHSRL 678
 S+ L M +L+ LR L DI+ RL + L L

Sbjct: 607 SVTRLCL-LQTLLEGCELCLRPRMSRLVQLRQLKANPDVIADIAKVGR-----IELQEL 662

Query: 679 KSLQVLVGAKFLVGGWRMEYLGEAHNLGSLSILELENVDRREAVKAKMREKNHVEQLS 738
 K+ V G + L + L+G LSI L+NV RE+ KA++ EK ++ L

Sbjct: 663 KAYNVDKKK----GHGIAELSAMNQLHGDSLIRNLQNVEKTRSRKARLDEKQKLKLD 717

Query: 739 LEWSESISADNSQTERDILDELRPDKNIKAVEITGYRGTFNFPNWADPLFVKLVHLYLRN 798
 L W++ A +R +L LRPH N++ + I Y GT+ P+W+ D + + LR+

Sbjct: 718 LRWADGRGAGECDRDRKVLKGLRPHPNLRELISIKYYGGTSSPSWMTDQYLPNMETIRLRS 777

Query: 799 CKDCYSLPALGQLPCLEFLSIRGMHGIRVVTTEFYGRLLSSKKPFNSLVKLRFEDMPEWKQ 858
 C LP LGQL L L I GM +R + FYG F L L MP ++

Sbjct: 778 CARLTELPCLGQLHILRHLHIDGMSQVRQINLQFYG-TGEVSGFPLLELLNIRRMPSEE 836

Query: 859 WH--TLGIGEFPTLEKLSIKNCPEL---SLEIPIQFSSLKRLDICDCKSVTSFPPSILP 912
 W FP L KL I++CP L SL ++ + R + D

Sbjct: 837 WSEPRRNCCYFPRLHKLLIEDCPRLRNLPSPPTLEELRISRTGLVLDLPGFHGNGDVTTN 896

Query: 913 TTLKRIKISGCPKLKLEAPVGEMFVEYLSVIDCGCVDDISPEFLP-----TARQLSI 964
 +L + +S C +L+ G + +++ D S EFLP + L +

Sbjct: 897 VSLSSLHVSECRELR-SLSEGLLQHNLVALKTAFTDCDSLEFLPAEGFRTAISLESIM 955

Query: 965 ENCHNVTRFLIPTATESLHIRNC-----EKLSMACGGAAQLTLSNIWGXXXXXX--- 1014
 NC FL+P++ E L ++ C + LS L+ L+I

Sbjct: 956 TNCPLPCSFLLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSLSFLDIKDCPNLSSFPPG 1015

Query: 1015 -XXXXXXXXTYCPEIEG---ELPFNLQILDIFYCKKL-----VNGRKEWHLQR 1062
 C ++ + +L+ L I+ C +L VN + L

Sbjct: 1016 PLCQLSALQHLSLVNCQRLQSIGFQALTSLESLTIQNCPRLTMSHSLVEVNNSSDTGLAF 1075

Query: 1063 LTELWIKHGSDEHIEHWELPSSIQRLFIFNLKTLSSQHLKSLTSQFLRIVG-NXXXXX 1121
 W++ D+ + L Q F L+ LT LQFL+I

Sbjct: 1076 NITRWMRRRTGDDGL---MLRHRAQNDSFF-----GGLLQHLTFLQFLKICQCPQLVTF 1126

Query: 1122 XXXXXXXXXHTSLQTLQIWNFLNXXXXXXXXXXXXX- ISNCPNLQSLPLKGMPSS 1180
 +LTSLQ L I + N + I CP + + P G+ S

Sbjct: 1127 TGEEEKWRNLTSQILHIVDCPNLEVLPANLQSLCSLSTLYIVRCPRIHAFFFFGGVSMS 1186

Query: 1181 LSTLSISKCPPLTPLEFDKGEYWTEIAHIPTI 1213
 L+ L I +CP L + G+ W IA++P I

Sbjct: 1187 LAHLVIHECPQLCQRCDDPVGDDWPLIANVPRI 1219

CPU time: 0.09 user secs. 0.01 sys. secs 0.10 total secs.

Lambda	K	H
0.320	0.137	0.406

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 9918
 Number of extensions: 6581
 Number of successful extensions: 26
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1220
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1078
Effective length of database: 765,046,036
Effective search space: 824719626808
Effective search space used: 824719626808
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter Align

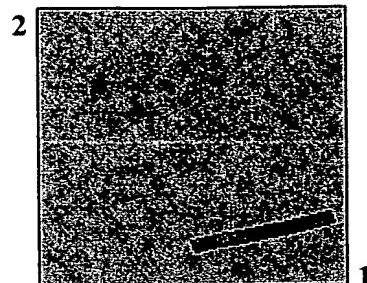
Nov Art

Claimed

D5

~~BB~~ 1 DNO:2

Sequence 1 lcl|seq_1 Length 318 (1 .. 318)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 34.3 bits (77), Expect = 6.9

Identities = 31/149 (20%), Positives = 66/149 (43%), Gaps = 6/149 (4%)

Query: 159 SIIGVHGLGGVGXXXXXXXXXXXXXXRDYHVVIMIEVANSETLNVDMQK-IIANRLA 217
S++ + G+GGVG +H+ + + V S+ NV + K II +
Sbjct: 205 SVLPLVGIGGVGKTTLAQLVYNDNRVGNY-FHLKVWVCV--SDNFNVKRLTKEIIESATK 261

Query: 218 LPWNESETERERSTYLRRALRRKKFVVLDDVW-KKFQLADVGIPTPSSDKGCKLILAS 275
+ ++ L+ + ++F++LDDVW + + P + +G K+I+ +
Sbjct: 262 VEQSDKLNLDTLQQILKEKIASERFLLVLDVVSENRDDWERLCAPLRFAARGSKVIVTT 321

Query: 276 RSNQVCVEMGDKEPMEMPCLGDNESLRLF 304
R ++ +G + + + L D+ LF

Sbjct: 322 RDTKIASIIGTMKEISLDGLQDDAYWELF 350

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda K H
0.319 0.135 0.400

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 2615
Number of extensions: 1870
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 0
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 1
Length of query: 318

Blast Result

Length of database: 765,046,178
Length adjustment: 130
Effective length of query: 188
Effective length of database: 765,046,048
Effective search space: 143828657024
Effective search space used: 143828657024
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 76 (33.9 bits)



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 | Filter Align

Print

Claimed

D5

SOA ID NO: 4

Sequence 1 lcl|seq_1 Length 318

Sequence 2 lcl|seq_2 Length 1232

No significant similarity was found

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